### - 12 -REMARKS

Claims 23-31, 34-42 and 51 stand rejected in the 02/28/2007 Office action, and claims 32, 33 and 43-50 stand withdrawn in that Office action. Claims 23-51 are cancelled herein, and new claims 52 to 75 are added herein. The relationships of these claims are summarized in the following section.

### Restriction/Election and Summary of Claim Relationships:

The 02/28/2007 Office action maintained the restriction based on lack of inventive step although acknowledging that the traversal arguments were persuasive as to the novelty of the technical feature linking the claims. However, in view of the dependency of the new claims, per below, and the amendments to the new independent claims, it is believed that this stated lack of inventive step is overcome. Accordingly, Applicant respectfully requests reconsideration of this restriction, believing further that it may be moot in view of the new claims are arguments herein.

Claims 52 and 53 directly derive from previously filed claims 23 and 24 however now limited to the 7S basic globulin sequences of the promoter and the leader (SEQ ID 6 and 7).

<u>Claims 54 and 55</u> directly derive from previously filed claims 26 and 27 as well restricted to the 7S basic globulin sequences of the promoter and the leader (SEQ ID 6 and 7).

Claims 56-58 directly derive from previously filed claims 29-31 as well restricted to the 7S basic globulin sequences of the promoter and the leader (SEO ID 6 and 7).

<u>Claims 59 and 60</u> derive from previously filed claims 32 and 33, but are now restricted to be dependent from claim 52 and 59 respectively, therefore also restricted to the 7S basic globulin sequences of the promoter and the leader (SEQ ID 6 and 7).

<u>Claims 61 and 62</u> directly derive from previously filed claims 34 and 35 and are now restricted to the 7S basic globulin sequences of the promoter and the leader (SEQ ID 6 and 7). <u>Claims 63-65</u> directly derive from previously filed claims 37-39 as well restricted to the 7S basic globulin sequences of the promoter and the leader (SEQ ID 6 and 7).

<u>Claims 66 and 67</u> directly derive from previously filed claims 41 and 42 as well restricted to the 7S basic globulin sequences of the promoter and the leader (SEQ ID 6 and 7).

Claims 68-70 and 72-75 derive from previously filed claims 43-45 and 47-50, but are now restricted to be dependent from claim 61, therefore also restricted to the 7S basic globulin sequences of the promoter and the leader (SEO ID 6 and 7).

Claim 71 derives from previously filed claim 51, also restricted to the 7S basic globulin sequences of the promoter and the leader (SEQ ID 6 and 7) and comprising steps as requested in a method claim.

The reasoning for now meeting the inventive step through the presentation of the claim set herein is provided in the following section.

# Introductory Discussion of Distinctions in the Art Field:

Prior proceeding with the examination, the examiner is kindly requested to take into account the following considerations.

The examiner has raised an objection based on the fact that "7S soy globulin gene" regulating sequences were claimed, and that  $\beta$ -conglycinine and 7S soy globulin appear to be the same gene.

However, as well described through all the specification, as well as in the sequence listing, the SEQ IDs No 6 and 7, are found in the <u>7S soy basic globulin</u> gene. This gene is completely different and has a completely different promoter, from the 7S soy globulin gene.

# The prior art for the 7S globulins from soybean can be summarized as follows:

The leguminosae storage proteins are divided in two classes: globulins and lectins.

The globulin class in turn is subdivided into two subclasses: legumins (11S hexameric proteins) and vicilins (7S trimeric or dimeric proteins).

β-conglycinine and basic 7S globulin, whose regulation elements were used to perform tissue-specific expression in seed (Sewry et al., 1995. The Plant Cell 7:945-956) belong to the vicillin subclass, but whereas the former was studied in detail, no detailed information is available on the 7S basic globulin functioning. β-conglycinine is a storage protein of the soybean, consisting of three different subunits,  $\alpha$ ,  $\alpha'$ ,  $\beta$  that interact non-covalently to form a trimer complex. The subunits are coded by a multigene family of 15 genes grouped in six nuclear DNA regions, whose expression is strictly regulated so as to be modulated during the plant life (Harada et al. 1989. The Plant Cell 1:415-425), Control is tissue-specific as well as stage-specific. In fact, the expression of each subunit is activated at high levels at the moment of embryo development, from the hearth shaped phase until complete ripening. The regulation of subunits  $\alpha/\alpha$  and  $\beta$  expression occur at a transcriptional as well as post-transcriptional level (Harada et al. 1989. The Plant Cell 1:415-425), and the  $\alpha$ ' subunit, of 76 KDa, is accumulated more precociously and in a larger amount as compared to B subunit. This behavior is due to the greater strength of the  $\alpha$ ' subunit due to the presence of an enhancer region, absent in  $\beta$ . and of a sequence stabilizing the a' transcript.

7S basic globulin, is a storage protein of soybean, with a high methionine and cysteine content. It is completely different from  $\beta$ -conglycinin as also shown in the annexed sequence alignments (provided herein as Exhibits 1 and 2) that were made with the two programs BLAST 2 and MULTALIN with the two sequences downloaded from the genbank database. Consideration of this evidence is respectfully requested as to the issues discussed herein.

In both alignments, the first results are on the complete sequences, the second results are on the alignment of the promoters from position 1 to the ATG codon, the third results are on the alignment of the coding sequences.

Like β-conglycinine, the 7S basic globulin (Bg) also is stored in seed in large amounts. It consists of two subunits, one of 27 KDa, the other of 16 KDa encoded by the same mRNA. Bg is synthesized as sole precursor polypeptide consisting of a putative peptide signal and of two subunits. In the genome about four copies of the Bg gene are present (Watanabe and Hirano, 1994. Plant Phys. 105:1019-1020). This

protein is mainly located in the seed embryonal tissues and its expression pattern is unusual for a storage protein (Nishizava et al. 1994. Plant Cell Physiol. 35:1079-1085). This location suggests that the Bg is not a mere storage protein, having other functions as well. More accurate data on Bg location and expression period in soybean are not available.

SEQ ID NO:6 and SEQ ID NO:7 are the first example of the 7S basic globulin "family of genes" and more accurate data on Bg location and expression period in soybean are not available. In the prior art, it has never been verified whether the site- and time-specific expression mechanism of the 7S basic globulin is preserved in other transformed plant species (like tobacco), furthermore the prior art does not teaches that the 7S basic globulin from soybean is equivalent to β-conglycinin (see Watanabe and Hirano (1994), Harada (1989) and Nishizava (1994)). The prior art teaches that the 7S basic globulin (Bg) consists of two subunits, one of 27 KDa, the other of 16 KDa encoded by the same mRNA. Bg is synthesized as sole precursor polypeptide consisting of a putative peptide signal and of two subunits. In the genome about four copies of the Bg gene are present (Watanabe and Hirano, 1994. Plant Phys. 105:1019-1020).

Thus, the promoter SEQ ID NO:6 and the signal sequence SEQ ID NO:7 are different, both at level of expression pattern and tissue accumulation (see Watanabe and Hirano (1994), Harada (1989) and Nishizava (1994)), from the well described β-conglycinin. It would be, very difficult for the skilled person, to predict whether the 7S basic globulin regulating elements could provide for the in seed expression of lysosomal enzymes in active form, as there are no indications in the prior art that expression vectors comprising the said regulating elements could provide expression of active enzymes in plant.

#### Objections to the Specification:

Applicants have amended the noted paragraphs of the specification, and the Abstract, to overcome the objections. Also, a similar inadvertent symbol error was noted in paragraph 0122 beginning on page 28, line 21 and this is corrected herein.

Applicants respectfully request withdrawal of the objections.

### Objections to the Claims:

Applicants have incorporated the requested changes to the new claims where appropriate, noting however that some of the requested changes to claims 23 and 34 (see new claims 52 and 61) were not added based on other changes to these claims. However, the objected to language is no longer present. Applicants respectfully request withdrawal of these objections where such objections are not moot.

### Rejection of the previously filed claims under 35 USC §112 and 101.

In compliance with the objections raised by the examiner concerning the failure to comply with the written description requirement, all the presently filed claims have been drafted taking into account the said objections. The claims have thus been amended in order be restricted to the embodiment wherein SEQ ID No 6 and 7 are used as regulating elements for the carrying out of the invention. The claims presently filed, hence, comply with the requirement of 35USC §§ 112 and 101. Withdrawal of these claim rejections is respectfully requested.

## Rejection of the previously filed claims under 35 USC §103.

Although acknowledging the compliance with the Novelty requirements of the previously filed claims, the said claims have been rejected by the examiner for lack of inventiveness based on the fact that Radin et al. allegedly teach transgenic tobacco plants expressing lysosomal enzymes and seeds of such plants.

The examiner also points out that Radin et al. do not teach the regulating sequences of 7S soy globulin nor an expression amount in seed of at least 0.8% of the total proteins of the seed.

The examiner also cites Chen et al, for the teaching of constructs comprising different fragments of the promoter from the  $\alpha'$  subunit gene being a 7S globulin protein and transgenic plants using the said promoter for a high accumulation in seed of certain proteins.

First of all it is herein noted that, although Radin et al. describes the expression of some lysosomal enzymes in tobacco plants, these enzymes are <a href="mailto:produced essentially in leaf">produced essentially in leaf</a> by plants transformed via the use of vectors containing the MeGa promoter or the cauliflower mosaic virus 35S promoter.

Although allegedly claiming also in-seed expression with the 35S promoter or with several inducible promoters, only demonstrates the use of the sole MeGa promoter for the in-leaf expression of GC and never demonstrates the possibility of an in-seed expression of said enzymes. The promoters cited by Radin et al, however, are not functional in-seed (as also proved by the applicant for the 35S promoter in figure 12 for the present application).

Hence, the document of Radin et al. does not teach the expression of lysosomal enzymes in seeds, as it does not even teach a promoter of a plant gene specific for the expression in seed storage organs and stage specific, nor does it teach an in seed (as it does not teach in seed expression) expression in an amount of at least 0.8% of total proteins of the seed, nor does it teach or even suggest: a promoter from a 7S soy globulin gene or a signal sequence from a 7S soy globulin protein, a promoter from a soy 7S basic globulin gene or a signal sequence from a soy 7S basic globulin protein.

Secondly, Chen at al, although teaching the expression pattern of the  $\beta$ -conglycinine  $\alpha'$  subunit protein in transgenic plants and its high expression level (0.1-5% of the proteins extracted from the seeds), also demonstrates at the same time (cfr. page 115 column 2 lines) that the  $\beta$  subunit of the same protein has an expression pattern 10-15 fold less than the  $\alpha'$  subunit of the same protein, in contrast with the  $\beta$  subunit of the phaseolin gene, thus pointing out the unpredictability of the expression pattern among 78 globulin genes.

An expression of 10 fold less would be 0.01-0.5% of the proteins extracted from the seeds and an expression of 15 fold less would be 0.005-0.25% of the proteins extracted from the seeds, which is well below the "at least 0.8%" claimed in the present application.

The paper published by Chen et al., hence, shows that "equivalent" subunits of

similar genes do not provide for the same expression patterns as it would be expected.

The paper is silent on the expression or on the possibility of the expression in seed of active enzymes using  $\beta$  conglycinine promoters.

The mere expression study and the localization of a seed protein in seeds of transgenic plants does not give guidance to the person skilled in the art for the possibility of using regulating elements of the said proteins for the expression of mammalian enzymes in an active form in seed.

The Chen et al. paper is also silent about the expression patterns and about the identification of the regulating sequences of the soy 7S basic globulin regulating regions

Whitelam discusses "bio-farming" in general and teaches that there are advantages to seed-localized expression of recombinant proteins but, at the time the application was filed, the use of specific promoters able to determine high levels of recombinant protein accumulation in specific compartments of the seed, stability of the protein and post-translational modifications was not obvious also to the person skilled in the art as above discussed.

In fact, Whitelam basically poses the problem solved by the present invention.

There were, at the time of filing of the application

a. no teachings of the promoters available for an in seed highly efficient expression of enzymes

b. no teachings that the soy 7S basic globulin promoter and leader sequences could have provided an efficient system in order to solve the problem posed by the Whitelam publication.

The unpredictability of the expression pattern of "equivalent" regions of similar genes highlighted by Chen et al, does not allow the person skilled in the art to expect the results obtained by the applicant by using soy 7S basic globulin regulating elements.

Furthermore, the lack of knowledge of the seed compartment wherein the leader sequence of the said gene vehicles the protein, did not allow the skilled person to consider obvious the expression of an heterologous enzyme in <u>active form</u> using the said sequence as regulating element for the expression of the said enzyme.

Moreover, the paper of Chang et al, proves that the skilled person cannot predict the expression levels of vincillin genes only on data regarding the expression pattern of genes or subunits of genes of the same family.

The soy 7S basic globulin, furthermore, is structurally different for the 7S soy genes, rendering any prediction even more impossible to make.

Based on the above arguments, it is herein believed that the presently filed claims cannot be considered obvious on the basis of the prior art cited and that they fulfill the requirements of 35 USC § 103 and that a patent should be granted with the said claims.

Applicants therefore respectfully request withdrawal of all claim rejections.

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Having overcome all rejections and objections, Applicants respectfully request that a timely Notice of Allowance be issued in this case.

The Examiner is invited to call the undersigned if clarification is needed on any aspects of this Reply/Amendment, or if the Examiner believes a telephonic interview would expedite the prosecution of the subject application to completion.

Respectfully submitted,

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	2541 2530	2620	2639	2649	2150	2664	2679	2500	2530	DW0	2710	2720 2730	
823750,1150Y895P	CTCSSIGGES	MALLE COLUMN	CICATCACTAC	TECHNICI	ACT CHARTA	CALLED STATE	TICTION CT	TOCCOM!	K FEDATAN	COMMITTEE	MICHITICAN	ATHERTET 6C TIL NO MEET TEEK MEET TE No Meet T. 6C TIL	ė
***************************************	2731 2740	2750	2750	2779	2780	2790	2900	2810	2000	2930	2940	2850 2860	
036267,1190798875 813759,115078757	TTELMETIO	-MONG	MICTAC INCAL	OTTATOS	-TIANTAN	TGTTUT MATE	NOCT BROATT	MACACIT II	OCTION IN	TANTAT—	MICHITATION	TITCETTETTC MATER	į
Concension	TiTegeditis		ATTENDED	GeseTiff			<b>ETColubing</b>	- Canada	MCTableta 2000	effection.	2970	IIII glog on sanist	٠
	7961 7970	2000	2050	2939	2900	2020	2830	2940		2960		TACETICCIENTO MAN	ì
038367,1150Y50G75 H13758,1150Y8P5P Consensus	SPECTIONS	TOWNSTOCT COM	ATTENTACTION OF THE	COCTOCTT	ETTCPCMM	armound t	CTITIONS CTITIONS	CREATION.	THE TORRA	OCCATIONTES	THE PART OF	Transportation for the	i
	2981 2000	3018	3029	2030	2040	3160	3160	3020	3001	3090	2100	21.20 21.20	•
015107,1150Y50G75 N12750,1150Y9F5F	TREETTEECC	NEW ISTOCAGE	SCOTEMBET IN	CHATTATAGE	TTTCHEN-	HORITTINI HOMEOCITIO	MATERIAL PROPERTY.	MATTER TEAT	T-FETTMEST	CHICTITATE MANAGEMENT	PROPERTY AND THE	ON THE TRANSPORT IN THE CO.	ė
Concensus	2121 2120	2149	2110	2109	3179	igClannTing 3180	akar Hages 1190	Maal Reflec	I delegal	Wiscongill a	2020	2040 2050	:
016107_1150750075								OC I FROCESS	Continu	OF LEMENTS	MATTERIA	TATATETT THE TTEM	í
016107,1197750375 813759,11979757 Cenemous	THIS CTOR	THE	Telegation of	Tie. Tellen	Talanalec		references	oc Feedfeel	ACRIENTI P	of feeders	octoo Telef		:
	3251 3250	3270	XTO	279	3300	331.0	3329	3330	2340	2290	3360	2270 2200	ŧ
016107,1150758678 813758,115078757	CTTRETTTT	THE IT IS THE	TINCKTETOR	MATTECATICES MERINACETUR	CIMACINI	CONNETTER	CECT TRITCAT	MITTITETAN	STICENS NO	CHITCHI	PECCHELLING	CIUTIA INCICIN	ė
Consensus	2001 2250		2410	Milesoni Milesoni	3430 3430	scamifeces 3440	antplical Min	mar r Filedly 3450	MOD	3400	3690	3500 251	
016107,1150750675					HUR PURSO	ici						SOUTCETTETCTICA	•
H13759,1158759575 Concentrate	CTRCGTTCC CTgcC al C		MICHTER TORC	ANCET METAN	MARK -COMMO	kq		CTCAGCCTCS					
	3511 3520	3530	2540	3550	2560	3570	2589	2000	3500	3610	XX	300 364	ŧ
016107,1190YSB575 H12755,1150YSPSP	TTTTEMENT	TTTTINCTONI	MOTETOTEC	ACTIMATED	WTDCT618A1	INSCIDATIONS	MECHANIA	MINTERNA	INTIME	MACTICAL	TCCATCIATE	AA CIMATAWATCHICA	đ
Consensor	X41 X50	30002											•
016107,1150F58675 812758.1158F8P5P		I STITIATATA											
(	AIGHTEETTT	I I I I I I I I I I I I I I I I I I I											

	1 10	20	30	49	50	60	70	80	90	100	110	120	130
besis beta-conglycinin Consensus	GARTGCGAAGA	REGTCRAATTCC	ACGRECACGA	CCACARCACO	COGREGAGES	ACGTCAGCAR	CACGETERGE	AGGAGGAAGA	CGRAGGTGRE	CASCCACGTC	CATTCCCATT	CCCRCGCCCA	CECCARC
	131 140	150	160	170	180	190	200	210	220	230	240	250	260
basic beta-conglycinin Consensus	СТСЯТСЯЯБЯБ	GRREAGCACGAG	CAGARGEAGG	ARCACEMATE	GCATCGCAAG	GAGGARARAC	ACGGRGGARA	GGGANGTGNA	GAGGANCAAG	ATGANCGTGA	ACACCCACGO	CONCRECANE	CTCATCA
	261 270	280	290	300	310	320	330	340	350	360	370	310	394
beric beto-conglycinin Consensus	AAAGGAAGAGA	RARRECREGART	GGCRACACAA	GCAGGRANAG			AGAAGAAGAA		ACGAGGATGA	GGRGCANGAC	RARGAGAGCO	ARGARAGTGA	RESTICT
	391 400	410	420	439	440	450	460	470	480	490	500	510	520
basic bete-conglyclmin Consensus	GAGTCTCARAG	RGRACCACGARG	ACRTANGART	RAGRACCETT	TTCACTTCAG	CTCTARRAGE	TRECRAGERE TTECRARCTE TACCARACAE	TETTCARRE	CCRRTRIGGO	CRCCCRR CRCGTTCGCG CRCCcna	TECTECAGAG	STICARCAGA	CACCCAC CACCCAC
	521 530	540	550	560	570	590	590	600	610	620	630	640	650
basic bata-conglyclnin Consensus	CRRTGCCTCR6 RRCRGCTTCR6 aReaGCcTCR6	TTGCCCCGCGGC RRTCTCCGAGAC aagCcCCGaGaC	ATCA-AGGC TACCGCATTT DaCaAggc	CAGASTACCA TAGASTTCAA CAGAGTgCAA	CAR-RANCEC CTCCAMACCO Can. RANCOC	ARCACCCTTC ARCACCCCTTC ARCACCCCTTC	ATETICENCES TTCTCCCCCS aTcTCCaCcfi	NTCCCNTCAC CCATGCTGAC lacaccaTcAC	CCANCARACE GCTGATTACE GCGGGGGGGGG	OFFITGORES TORTOSTRAT SCREENS	ARCTRGGF CCTTRACGG BBCTRGGF	GRAGACGTTC ACTGCCATTC aaaGeCaTTC	TTGCRRT TTRCCTT TTaCeeT
	651 660	670	680	650	700	710	720	730	740	750	760	770	780
hasic beta-conglyclmin Conscnaus	RETERRERER	CCRCRCRAGGGT RCGRCCGAGACT aCasaCaR6acT	CTTRCSSCCT	TORRICTEGO	RATECCCTAR	RRETCCCTEC	REGRACCRES	TTCTATGTGG	TTRACCCTOR	CARCGACGAG	BATCTCAGGE	TGRTAGCAGG	RACCACA
	781 790	800	810	820	830	840	850	860	870	880	890	900	910
basic beta-conglycinin Consensus	TTCTATGTGGT	TGGETTRGGCCR TRRCCCTGRCRR TaacooaGaCaR	CG-ACGAGAA	TCTCREAMIG	RYMACACTCG	CCRTACCCGT	TARCARACCE	GGTAGATTTE	REAGTTTCTT	CCTATCTAGO	<b>PICTORAGETO</b>	RACAGTCCTR	CTTGCAA CTagaAa
	911 920	930	940	950	960	970	980	550	1000	1010	1020	1030	1040
besic beta-conglycinin Consensus	<b>GGGTTCRGCRB</b>	GATECRECTARO GARTATTETAGA GAegaacCTRas	B <b>ecctca</b> tac	GACACCAAAT	TCGAGGAGAT	RESCRIPTION	CTGTTTSSTR	GAGAGGAGGG	GCAGCAACAA	GEGERGGRER	GGCTGCAAGE	GRETGTERTT	GTEGRAA
	1041 1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
basio bete-conglycinin Consensus	TETERHIGRAR	CARCCAGCA CARATTCGGGAA CARCcaGaA	CTGREC BRRC	REGUERRATIC	DESTICEMENT	RESECCETTE	CTICTGREGS	TRARCCITTC	ARCYTEGERA	RECECCIAC-	+CCCRTCTRI	TOOR+ROHAG	CITESCS
	1171 1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
basic beta-conglycinin Consensus	<b>SCITGITTESC</b>	TACCAGGCT RTTACCCAGAGA aaCCAGaga	ARCCCT CRGC	TTC0568CIT	SERTSTETTE	CTCSSTSTTE	TEESTRIESS	CORGUODSCT	CTTITICTAC	CRICICT FORM	TICHRAGECO	RTAGTESTAC	GAT TAGTUAT
	1301 1310	1320	1339	1349	1350	1360	1370	1390	1390	1400	1410	1420	1430
basio beta-conglycinin Consensus	TRRICANGERO	RTCCTRGCRTGG RASCARIACRITG RacCarlaCaTgG	HACTIGITEG	CRITTHERGRE	CHRICARICAGE	GGTCCT GGCRGCBRICH GGaaCa	GERNEAGERE	CCTTIGGRAG	TECHERRRIFE	<b>IRGRICTIONS</b>	LISTCTERRO	ASSCACARCE FERSITATET T Researance	ETRA1C
	1431 1440	1450	1460	1470	1490	1490	1500	1510	1520	1530	1540	1550	1560
besic bete-conglyclnin Consensus	CCRGCRGGT	TGTTRTGRRTGG TRTCCAGTTRTG TaTcaaGaaag6	STCRACECTA	CCTCREATER	GARTITCT	TIGCITTIGE	TRICARISCE	GREARCARCE	AGREGARCT	CCTTGCRGGT	TEGRARGACE	RIGIGATANG	CAGATA
	1561 1570	1580	1599	1600	1610	1620	1630	1640	1650	1560	1670	1680	1690
basic beta-conglycinin Come ensus	CCTAGTCAAGT	SCRETCGCATGG SCREGAGCTTGO SCREGAGCATGC	STTCCCTRGG	TCT6C88888	RTRITERGRA	CCTARTARAS	TECCRATECA AGCCARAGTE AGCCARAGCE	RETCCTRCTT	TETEGATECT	CAGCC YCAGO	ASAAAGAGG	GGGGAACAAG	SERRGAR
	1651 1700	1710	1720	1728									
bete-conglyclnin Consensus	REGETCETTTE	TETTERATTTTG	eggc11111	ACTGA									

CODING SEQUENCE: Basic (D16107); beta-conglycinin (M13759)

	1	10	20	30	40	50	60	70	80	90	100	110	120	13
016107,11PROM H13759,11PROM Consensus	GGTTI								ANATCHARAT					
	131	140	150	160	170	180	190	200	210	220	230	240	250	26
016107,11PROM H13759,11PROM Concentrue	AACR	TRITIONAL TTITCARN	ARGRETTTS TTGRETTTT	RATGIGIGIA	<b>GTRAGTATRA</b>	ATT TRABBITTE	HAR-TARK	<b>ACRETTATI</b>	RRTCTTGGRG TRTCRARRTG aATCaaaaa6	SCR <b>RRR</b> ACRT	TIBBT	ACGTATTATT	TRITTERREAGE	CTRARA
	261	270	280	290	300	310	320	330	340	350	360	370	380	39
016107,11PROH H13759,11PROH Concensus	BTBB	ETETREEST	TITTERTET	CTRITCTTAT	GTATTITTE	MORTC TRIT	TRIBITGAT	CRAC-TAR	AACAGTTGAA AATATTTTA AACAgTTgaA	SCSCRTCRCT FATCTRCRCT	CASCASSC TA		-TITTGCATT	TITET
	391	400	410	420	430	440	450	460	470	460	490	500	510	52
016107.11PROM H13759,11PROM Concensus	CRRT	IICDE	CETTITIE	GC	RIBIT ISSTE	HEACHAITE	TT88	-IBBTCBBTC	TCRCTTCTTR RTTRTTCTTR acaaTTCTTR	RIGGIACAL	RITETTERA	CCRTRIGRAG	ISTICSTING	TARAGA
	521	530	540	550	560	570	580	590	200	610	620	630	640	65
D16107.11PRON H13759.11PRON Consensus	TATG	TRARARATE -GGRTAGTE - aaRafa T	Tal Taa TeO	RTREATRE REGCCTTCR RTacaaTacR	Ta	-10000018 .TGCCaaTe	TRRITRRTT Faransa	TGG1FINCHGR gaaTRRafiafi	ATRANTAGAR TTCGTTCTRR aTasaTagAR	CHETTACTT	RRICCTICCI RRescyanal	CATCHTRATT CASARABATT	ARTCIGGTHG aaacy66gRc	RRRTARI TTCGRR anagAR
	651	560	670	680	630	700	710	720	730	740	750	760	770	78
016107,11PROM H13759,11PROM Consensus	ROOM	PRIBLIES	PRETITION	DONCESTRAGE	ABBSBECC	MC(394C889	TERRETERIN	<b>PURCENTERS</b>	AGATACACAA AGTATECTITI AGAAACacga	CRINGCORT	STCTHAGITO	KIRRI	RTICHARCHA	BHEFTE
	781	790	800	810	620	830	849	850	860	870	880	830	900	91
016107,11PROH H13759,11PROH Consensus	ATCRC	RAGACAMAR RC-RCAGTO	SACATCACT	TATICACTAG	CTGAT	RESERVECO	CSTC9	- AGRARAGAA	RACGENTERA RAC TEGA RAC TEGAR	COCCAARREC	CATECA-CAS	CRACAC-STA	CTCRCRR——	RRSTAC
		920	930	940	\$50	360	970	30)	390	1000	1010	1020	1030	104
	311												corroccor	emona
016107,1 IPROM H13759,1 IPROM Consensus	CCTCF	CRCTCRCCR	BARCATTCA	TTTCTCCCC CORCTCARC CRACTCARC	RTTGCRTGTT	ACT CRACT T	PATERTIE	9800	RARTTTCRCRI CHRCCTCRRRI ARROCTCRARI	TICET-BITC	TOTTOCROOM	CTERTITIE	STITTETTTCS	aCaass
H13759.1   PROM	CCTCF MITCE aaTCa	ICRCTCHCCH HIGCRGCCCH HACCGCGCCCT	BARCATTCA	CONSCITUTE OF THE PROPERTY I	RTTGCRTGTT	ACT CRACT T	PATERTIE	9800	CHRCCTERRA ARRESTERAR 1120	TCGT-ATTC agCeT_ReaC	TCTTCCSCCA aCgTCcaCcal 1140	CTCRTTTTT ConncTTgT 1150	GITTATITCA GeccReceCe 1160	aCaaaaa 1170
H13759.1   PROM	1041 GRARE TERRE	CRCTCHCCH HIGCHSCCCH MACOCACCH 1050	ARRCRITCA FlaaCaTTca 1060 ATCCCGTTO ACCCCGTGS	TTTTCTCCCC CCARCTCARC CCARCTCARC 1070 RCRCTTAGCC CCARRTETTO	RTTSCRTGTT CCRTCATGAS ACAGCRTGAS 1080 ACTTRANSCTT B-TSCRTGTT	MCTCHRGTT XXRCHCRTT MCGCRGGTT 1030 MCCCRRRCGG MCRRGGC	TATECTTICT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT	1110	CHRCCTERRA ARROTOSHRA	1130 CCRESTITE	TCTTCCGCCA aCgTCcaCcal 1140 CACTACCATT CATCATCAGG	1150 TITCHRITTI	GETTATTTCR GeccReceCe 1160 CRANCCTTGC	1170 TCTRTRI
M13759.1   PROM Consensus D16107.1   PROM H13759.1   PROM	1041 1041 1041 1041 1041 1171	CRCTCHCCH HIGCHSCCCH MACOCACCH 1050	RANCATTCA FlanCaTTCA 1060 RTCCCGTTO RCCCCGTGG ReCCCGTgc-	TTTTCTCCCC CCARCTCARC CCARCTCARC 1070 RCRCTTAGCC CCARRTETTO	RTTSCRTGTT CCRTCATGAS ACAGCRTGAS 1080 ACTTRANSCTT B-TSCRTGTT	MCTCHRGTT XXRCHCRTT MCGCRGGTT 1030 MCCCRRRCGG MCRRGGC	TATECTTICT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT TGTTGTTTCT	1110	CHACCTCHARA ARROCTCHARA 1120 TAGCTCTCTARA	1130 CCRESTITE	TCTTCCGCCA aCgTCcaCcal 1140 CACTACCATT CATCATCAGG	1150 TITCHRITTI	GETTATTTCR GeccReceCe 1160 CRANCCTTGC	1170 TCTRTRI

FROM 1 TO ATG